

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/902,516DATE: 11/25/98  
TIME: 18:41:18

INPUT SET: S29984.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

ENTERED

## SEQUENCE LISTING

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Soo Hoo, William  
6  
7 (ii) TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
8 COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
9 RESPONSE USING SAME  
10  
11 (iii) NUMBER OF SEQUENCES: 50  
12  
13 (iv) CORRESPONDENCE ADDRESS:  
14 (A) ADDRESSEE: CAMPBELL & FLORES, LLP  
15 (B) STREET: 4370 La Jolla Village Drive, Suite 700  
16 (C) CITY: San Diego  
17 (D) STATE: California  
18 (E) COUNTRY: United States  
19 (F) ZIP: 92121  
20  
21 (v) COMPUTER READABLE FORM:  
22 (A) MEDIUM TYPE: Floppy disk  
23 (B) COMPUTER: IBM PC compatible  
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
26  
27 (vi) CURRENT APPLICATION DATA:  
28 (A) APPLICATION NUMBER: US 08/902,516  
29 (B) FILING DATE: 29-JUL-1997  
30 (C) CLASSIFICATION:  
31  
32 (viii) ATTORNEY/AGENT INFORMATION:  
33 (A) NAME: Campbell, Cathryn A.  
34 (B) REGISTRATION NUMBER: 31,815  
35 (C) REFERENCE/DOCKET NUMBER: P-IM 2442  
36  
37 (ix) TELECOMMUNICATION INFORMATION:  
38 (A) TELEPHONE: (619)535-9001  
39 (B) TELEFAX: (619)535-8949  
40  
41  
42 (2) INFORMATION FOR SEQ ID NO:1:  
43  
44 (i) SEQUENCE CHARACTERISTICS:  
45 (A) LENGTH: 660 base pairs  
46 (B) TYPE: nucleic acid

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47 (C) STRANDEDNESS: both  
48 (D) TOPOLOGY: linear  
49  
50

51 (ix) FEATURE:  
52 (A) NAME/KEY: CDS  
53 (B) LOCATION: 1..660  
54  
55

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
57

58	ATG GAG ACA GAC ACA CTC CTG CTA TGG GTA CTG CTG CTC TGG GTT CCA	48
59	Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro	
60	1 5 10 15	
61		
62	GGT TCC ACT GGG GAC TAT CCA TAT GAT GTT CCA GAT TAT GCT GGG GCC	96
63	Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala	
64	20 25 30	
65		
66	CAA GCA CCC ACC CGC TCA CCC ATC ACT GTC ACC CGG CCT TGG AAG CAT	144
67	Gln Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His	
68	35 40 45	
69		
70	GTA GAG GCC ATC AAA GAA GCC CTG AAC CTC CTG GAT GAC ATG CCT GTC	192
71	Val Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val	
72	50 55 60	
73		
74	ACG TTG AAT GAA GAG GTA GAA GTC GTC TCT AAC GAG TTC TCC TTC AAG	240
75	Thr Leu Asn Glu Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys	
76	65 70 75 80	
77		
78	AAG CTA ACA TGT GTG CAG ACC CGC CTG AAG ATA TTC GAG CAG GGT CTA	288
79	Lys Leu Thr Cys Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu	
80	85 90 95	
81		
82	CGG GGC AAT TTC ACC AAA CTC AAG GGC GCC TTG AAC ATG ACA GCC AGC	336
83	Arg Gly Asn Phe Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser	
84	100 105 110	
85		
86	TAC TAC CAG ACA TAC TGC CCC CCA ACT CCG GAA ACG GAC TGT GAA ACA	384
87	Tyr Tyr Gln Thr Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr	
88	115 120 125	
89		
90	CAA GTT ACC ACC TAT GCG GAT TTC ATA GAC AGC CTT AAA ACC TTT CTG	432
91	Gln Val Thr Thr Tyr Ala Asp Phe Ile Asp Ser Leu Lys Thr Phe Leu	
92	130 135 140	
93		
94	ACT GAT ATC CCC TTT GAA TGC AAA AAA CCA GGC CAA AAA GTC GAC GAA	480
95	Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys Val Asp Glu	
96	145 150 155 160	
97		
98	CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC CAG GAC ACG	528
99	Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp Thr	

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100          165          170          175
101
102  CAG GAG GTC ATC GTG GTG CCA CAC TCC TTG CCC TTT AAG GTG GTG GTG      576
103  Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val Val
104          180          185          190
105
106  ATC TCA GCC ATC CTG GCC CTG GTG GTG CTC ACC ATC ATC TCC CTT ATC      624
107  Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser Leu Ile
108          195          200          205
109
110  ATC CTC ATC ATG CTT TGG CAG AAG AAG CCA CGT TAG      660
111  Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg
112          210          215          220
113
114
115  (2) INFORMATION FOR SEQ ID NO:2:
116
117      (i) SEQUENCE CHARACTERISTICS:
118          (A) LENGTH: 219 amino acids
119          (B) TYPE: amino acid
120          (D) TOPOLOGY: linear
121
122      (ii) MOLECULE TYPE: protein
123
124      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
125
126  Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
127      1          5          10          15
128
129  Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
130          20          25          30
131
132  Gln Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His
133          35          40          45
134
135  Val Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val
136          50          55          60
137
138  Thr Leu Asn Glu Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys
139      65          70          75          80
140
141  Lys Leu Thr Cys Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu
142          85          90          95
143
144  Arg Gly Asn Phe Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser
145          100          105          110
146
147  Tyr Tyr Gln Thr Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr
148          115          120          125
149
150  Gln Val Thr Thr Tyr Ala Asp Phe Ile Asp Ser Leu Lys Thr Phe Leu
151      130          135          140
152

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153 Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys Val Asp Glu
154 145                      150                      155                      160
155
156 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp Thr
157                      165                      170                      175
158
159 Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val Val
160                      180                      185                      190
161
162 Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser Leu Ile
163                      195                      200                      205
164
165 Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg
166 210                      215
167
168

```

(2) INFORMATION FOR SEQ ID NO:3:

```

171 (i) SEQUENCE CHARACTERISTICS:
172 (A) LENGTH: 9 amino acids
173 (B) TYPE: amino acid
174 (D) TOPOLOGY: linear
175

```

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

182 Val Gln Gly Glu Glu Ser Asn Asp Lys
183 1                      5
184

```

(2) INFORMATION FOR SEQ ID NO:4:

```

187 (i) SEQUENCE CHARACTERISTICS:
188 (A) LENGTH: 25 amino acids
189 (B) TYPE: amino acid
190 (D) TOPOLOGY: linear
191

```

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

198 Phe Ile Leu Pro Ile Leu Gly Ala Val Leu Ala Leu Leu Leu Leu
199 1                      5                      10                      15
200
201 Thr Leu Leu Ala Leu Leu Leu Leu Val
202                      20                      25
203

```

(2) INFORMATION FOR SEQ ID NO:5:

205

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206 (i) SEQUENCE CHARACTERISTICS:  
207 (A) LENGTH: 26 amino acids  
208 (B) TYPE: amino acid  
209 (D) TOPOLOGY: linear  
210  
211 (ii) MOLECULE TYPE: peptide  
212  
213  
214  
215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
216  
217 Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met Val  
218 1 5 10 15  
219  
220 Phe Val Ala Leu Leu Val Phe Tyr Ile Thr  
221 20 25  
222  
223 (2) INFORMATION FOR SEQ ID NO:6:  
224  
225 (i) SEQUENCE CHARACTERISTICS:  
226 (A) LENGTH: 22 amino acids  
227 (B) TYPE: amino acid  
228 (D) TOPOLOGY: linear  
229  
230 (ii) MOLECULE TYPE: peptide  
231  
232  
233  
234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
235  
236 Ala Leu Val Val Ile Pro Ile Ile Phe Gly Ile Leu Phe Ala Ile Leu  
237 1 5 10 15  
238  
239 Leu Val Leu Val Phe Ile  
240 20  
241  
242 (2) INFORMATION FOR SEQ ID NO:7:  
243  
244 (i) SEQUENCE CHARACTERISTICS:  
245 (A) LENGTH: 20 amino acids  
246 (B) TYPE: amino acid  
247 (D) TOPOLOGY: linear  
248  
249 (ii) MOLECULE TYPE: peptide  
250  
251  
252  
253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
254  
255 Ile Ser Gly Ala Thr Ala Gly Val Pro Thr Leu Leu Leu Gly Leu Val  
256 1 5 10 15  
257  
258 Leu Pro Ala Pro

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/902,516

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## \*\*\*\*\* PREVIOUSLY ERRORED SEQUENCES - EDITED \*\*\*\*\*

42 (2) INFORMATION FOR SEQ ID NO:1:

43

44 (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 660 base pairs

46 (B) TYPE: nucleic acid

47 (C) STRANDEDNESS: both

48 (D) TOPOLOGY: linear

49

50

51 (ix) FEATURE:

52 (A) NAME/KEY: CDS

53 (B) LOCATION: 1..660

54

55

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

57

58 ATG GAG ACA GAC ACA CTC CTG CTA TGG GTA CTG CTG CTC TGG GTT CCA 48

59 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro

60 1 5 10 15

61

62 GGT TCC ACT GGG GAC TAT CCA TAT GAT GTT CCA GAT TAT GCT GGG GCC 96

63 Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala

64 20 25 30

65

66 CAA GCA CCC ACC CGC TCA CCC ATC ACT GTC ACC CGG CCT TGG AAG CAT 144

67 Gln Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His

68 35 40 45

69

70 GTA GAG GCC ATC AAA GAA GCC CTG AAC CTC CTG GAT GAC ATG CCT GTC 192

71 Val Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val

72 50 55 60

73

74 ACG TTG AAT GAA GAG GTA GAA GTC GTC TCT AAC GAG TTC TCC TTC AAG 240

75 Thr Leu Asn Glu Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys

76 65 70 75 80

77

78 AAG CTA ACA TGT GTG CAG ACC CGC CTG AAG ATA TTC GAG CAG GGT CTA 288

79 Lys Leu Thr Cys Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu

80 85 90 95

81

82 CGG GGC AAT TTC ACC AAA CTC AAG GGC GCC TTG AAC ATG ACA GCC AGC 336

83 Arg Gly Asn Phe Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser

84 100 105 110

85

86 TAC TAC CAG ACA TAC TGC CCC CCA ACT CCG GAA ACG GAC TGT GAA ACA 384

87 Tyr Tyr Gln Thr Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr

88 115 120 125

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION** *US/08/902,516*

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[illegible]

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/902,516**

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Line

Error

Original Text